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RAW SEQUENCE LISTING

DATE: 05/03/2002

PATENT APPLICATION: US/09/997,977

TIME: 12:01:09

Input Set : N:\Crif3\RULE60\09997977.raw

Output Set: N:\CRF3\05032002\I997977.raw

3 <110> APPLICANT: Bartel, Paul L.
 4 Tavgigian, Sean V.
 5 Myriad Genetics, Inc.
 7 <120> TITLE OF INVENTION: MMSC1 - An MMAC1 Interacting Protein
 9 <130> FILE REFERENCE: MMSC1 Gene
 11 <140> CURRENT APPLICATION NUMBER: 09/997,977
 12 <141> CURRENT FILING DATE: 2001-12-03
 15 <150> PRIOR APPLICATION NUMBER: 09/233,086
 16 <151> PRIOR FILING DATE: 1999-01-19
 18 <150> PRIOR APPLICATION NUMBER: US 60/071,861
 19 <151> PRIOR FILING DATE: 1998-01-20
 21 <160> NUMBER OF SEQ ID NOS: 65
 23 <170> SOFTWARE: PatentIn Ver. 2.0
 25 <210> SEQ ID NO: 1
 26 <211> LENGTH: 4
 27 <212> TYPE: PRT
 28 <213> ORGANISM: Artificial Sequence
 30 <220> FEATURE:
 31 <223> OTHER INFORMATION: Description of Artificial Sequence:PDZ Consensus
 32 Domain
 34 <220> FEATURE:
 35 <221> NAME/KEY: PEPTIDE
 36 <222> LOCATION: (2)..(4)
 37 <223> OTHER INFORMATION: Xaa at residue 2 may be Ser or Thr; Xaa at residue
 38 3 may be any amino acid; Xaa at residue 4 may be
 39 Val or Ile.
 41 <400> SEQUENCE: 1
 W--> 42 Glu Xaa Xaa Xaa
 43 1
 46 <210> SEQ ID NO: 2
 47 <211> LENGTH: 5836
 48 <212> TYPE: DNA
 49 <213> ORGANISM: Homo sapiens
 51 <220> FEATURE:
 52 <221> NAME/KEY: CDS
 53 <222> LOCATION: (115)..(5757)
 55 <400> SEQUENCE: 2
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 58 tgctcctcca gcgcaccagg tgtctttaag agtgattgaa gagaataatt caaa atg 117
 59 Met
 60 1
 62 cct gaa aat cct gct aca gat aaa ctg cag gtg ctg cag gta ctt gat 165
 63 Pro Glu Asn Pro Ala Thr Asp Lys Leu Gln Val Leu Gln Val Leu Asp

ENTERED

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64	5	10	15	
66	cgc ctg aaa atg aaa ttg cag gag aag ggt gac acg tcg cag aat gag	213		
67	Arg Leu Lys Met Lys Leu Gln Glu Lys Gly Asp Thr Ser Gln Asn Glu			
68	20	25	30	
70	aag tta tct atg ttt tat gag aca cta aag agt cct ctc ttc aac cag	261		
71	Lys Leu Ser Met Phe Tyr Glu Thr Leu Lys Ser Pro Leu Phe Asn Gln			
72	35	40	45	
74	ata ctc aca ctt cag cag tcc atc aag caa ctg aag ggt caa ctc aac	309		
75	Ile Leu Thr Leu Gln Gln Ser Ile Lys Gln Leu Lys Gly Gln Leu Asn			
76	50	55	60	65
78	cat ata ccc tca gat tgt tca gcc aac ttt gat ttt tct agg aaa ggt	357		
79	His Ile Pro Ser Asp Cys Ser Ala Asn Phe Asp Phe Ser Arg Lys Gly			
80	70	75	80	
82	ttg tta gtg ttc aca gat ggt tcc att act aat gga aat gtc cac agg	405		
83	Leu Leu Val Phe Thr Asp Gly Ser Ile Thr Asn Gly Asn Val His Arg			
84	85	90	95	
86	ccc tct aat aac tcg act gta tct ggg tta ttt ccg tgg acc ccg aag	453		
87	Pro Ser Asn Ser Thr Val Ser Gly Leu Phe Pro Trp Thr Pro Lys			
88	100	105	110	
90	ttg gga aat gaa gac ttt aac tca gtc att caa cag atg gct cag ggc	501		
91	Leu Gly Asn Glu Asp Phe Asn Ser Val Ile Gln Gln Met Ala Gln Gly			
92	115	120	125	
94	cgg caa att gaa tat ata gat ata gaa cgg cct tca act gga ggc ctt	549		
95	Arg Gln Ile Glu Tyr Ile Asp Ile Glu Arg Pro Ser Thr Gly Gly Leu			
96	130	135	140	145
98	gga ttc agt gtg gtg gcc ctc aga agt caa aat ctc gga aaa gtt gat	597		
99	Gly Phe Ser Val Val Ala Leu Arg Ser Gln Asn Leu Gly Lys Val Asp			
100	150	155	160	
102	atc ttc gtg aag gat gtc cag cca ggg agt gta gca gac agg gat caa	645		
103	Ile Phe Val Lys Asp Val Gln Pro Gly Ser Val Ala Asp Arg Asp Gln			
104	165	170	175	
106	aga tta aag gaa aat gat caa ata ttg gcc att aat cac acg cca ttg	693		
107	Arg Leu Lys Glu Asn Asp Gln Ile Leu Ala Ile Asn His Thr Pro Leu			
108	180	185	190	
110	gat cag aac att tcc cat cag caa gca att gca tta tta caa caa acc	741		
111	Asp Gln Asn Ile Ser His Gln Gln Ala Ile Ala Leu Leu Gln Gln Thr			
112	195	200	205	
114	act gga tct ttg aga ctg att gtg gcc agg gaa cca gtc cac aca aaa	789		
115	Thr Gly Ser Leu Arg Leu Ile Val Ala Arg Glu Pro Val His Thr Lys			
116	210	215	220	225
118	agc agt act tct agc agc cta aat gat aca act ctg cct gaa aca gtt	837		
119	Ser Ser Thr Ser Ser Ser Leu Asn Asp Thr Thr Leu Pro Glu Thr Val			
120	230	235	240	
122	tgt tgg ggc cat gtt gaa gag gtt gag ctc att aat gat ggc tct gga	885		
123	Cys Trp Gly His Val Glu Glu Val Glu Leu Ile Asn Asp Gly Ser Gly			
124	245	250	255	
126	cta ggt ttt gga ata gtt gga gga aaa aca agt ggc gtg gtt gtg agg	933		
127	Leu Gly Phe Gly Ile Val Gly Gly Lys Thr Ser Gly Val Val Val Arg			
128	260	265	270	

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130	act	ata	gtt	cct	gga	gga	tta	gca	gat	cga	gat	gga	aga	ctc	cag	aca	981
131	Thr	Ile	Val	Pro	Gly	Gly	Leu	Ala	Asp	Arg	Asp	Gly	Arg	Leu	Gln	Thr	
132		275					280					285					
134	ggg	gac	cac	atc	ttg	aag	att	ggt	ggc	aca	aac	gtg	cag	gga	atg	acc	1029
135	Gly	Asp	His	Ile	Leu	Lys	Ile	Gly	Gly	Thr	Asn	Val	Gln	Gly	Met	Thr	
136	290					295					300					305	
138	agt	gag	caa	gtt	gca	caa	gtt	cta	agg	aac	tgt	ggg	aat	tca	gtc	agg	1077
139	Ser	Glu	Gln	Val	Ala	Gln	Val	Leu	Arg	Asn	Cys	Gly	Asn	Ser	Val	Arg	
140					310					315					320		
142	atg	ctc	gtt	gct	aga	gat	cca	gct	ggt	gac	att	tca	gtc	acc	ccc	cct	1125
143	Met	Leu	Val	Ala	Arg	Asp	Pro	Ala	Gly	Asp	Ile	Ser	Val	Thr	Pro	Pro	
144					325					330					335		
146	gcc	cct	gca	gcc	tta	cct	gtt	gcc	ctg	cct	act	gta	gcc	agc	aag	ggc	1173
147	Ala	Pro	Ala	Ala	Leu	Pro	Val	Ala	Leu	Pro	Thr	Val	Ala	Ser	Lys	Gly	
148			340						345					350			
150	cct	ggt	tct	gac	agt	tct	ctt	ttt	gaa	act	tat	aat	gtt	gag	ctt	gtg	1221
151	Pro	Gly	Ser	Asp	Ser	Ser	Leu	Phe	Glu	Thr	Tyr	Asn	Val	Glu	Leu	Val	
152		355					360					365					
154	aga	aaa	gat	ggg	cag	agt	ctt	gga	att	aga	att	gtt	ggc	tat	gtt	gga	1269
155	Arg	Lys	Asp	Gly	Gln	Ser	Leu	Gly	Ile	Arg	Ile	Val	Gly	Tyr	Val	Gly	
156	370					375					380					385	
158	aca	tct	cat	aca	ggg	gaa	gct	tca	ggg	att	tat	gtg	aaa	agt	gta	ata	1317
159	Thr	Ser	His	Thr	Gly	Glu	Ala	Ser	Gly	Ile	Tyr	Val	Lys	Ser	Val	Ile	
160					390					395					400		
162	cct	ggc	agt	gct	gcg	tac	cac	aat	ggc	cac	att	caa	gtg	aat	gac	aaa	1365
163	Pro	Gly	Ser	Ala	Ala	Tyr	His	Asn	Gly	His	Ile	Gln	Val	Asn	Asp	Lys	
164					405					410					415		
166	ata	gtt	gct	gtc	gat	ggc	gtg	aac	att	cag	ggt	ttt	gcc	aac	cat	gat	1413
167	Ile	Val	Ala	Val	Asp	Gly	Val	Asn	Ile	Gln	Gly	Phe	Ala	Asn	His	Asp	
168			420						425					430			
170	gtt	gtt	gaa	gta	tta	cga	aat	gca	ggg	cag	gtg	gta	cac	cta	acc	cta	1461
171	Val	Val	Glu	Val	Leu	Arg	Asn	Ala	Gly	Gln	Val	Val	His	Leu	Thr	Leu	
172		435					440					445					
174	gtt	cga	agg	aag	aca	tcc	tca	tct	act	tct	cca	ctt	gaa	cca	cct	tca	1509
175	Val	Arg	Arg	Lys	Thr	Ser	Ser	Ser	Thr	Ser	Pro	Leu	Glu	Pro	Pro	Ser	
176	450					455					460					465	
178	gac	aga	gga	act	gtt	gta	gaa	cca	ctg	aaa	cca	cca	gct	ctc	ttt	cta	1557
179	Asp	Arg	Gly	Thr	Val	Val	Glu	Pro	Leu	Lys	Pro	Pro	Ala	Leu	Phe	Leu	
180					470					475					480		
182	act	gga	gca	gtg	gaa	act	gaa	act	aat	gtg	gat	ggt	gaa	gat	gag	gaa	1605
183	Thr	Gly	Ala	Val	Glu	Thr	Glu	Thr	Asn	Val	Asp	Gly	Glu	Asp	Glu	Glu	
184					485					490					495		
186	att	aaa	gaa	aga	att	gat	act	tta	aaa	aat	gac	aac	ata	caa	gcc	tta	1653
187	Ile	Lys	Glu	Arg	Ile	Asp	Thr	Leu	Lys	Asn	Asp	Asn	Ile	Gln	Ala	Leu	
188			500						505					510			
190	gaa	aaa	ttg	gaa	aaa	gtc	cca	gac	tct	cca	gaa	aat	gag	ctg	aaa	tcc	1701
191	Glu	Lys	Leu	Glu	Lys	Val	Pro	Asp	Ser	Pro	Glu	Asn	Glu	Leu	Lys	Ser	
192		515						520				525					
194	aga	tgg	gaa	aac	ctg	ttg	ggt	cct	gat	tat	gaa	gta	atg	gtt	gct	act	1749

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195	Arg	Trp	Glu	Asn	Leu	Leu	Gly	Pro	Asp	Tyr	Glu	Val	Met	Val	Ala	Thr	
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198	ttg	gac	aca	cag	att	gca	gat	gat	gct	gag	tta	cag	aaa	tat	tca	aag	1797
199	Leu	Asp	Thr	Gln	Ile	Ala	Asp	Asp	Ala	Glu	Leu	Gln	Lys	Tyr	Ser	Lys	
200					550					555					560		
202	ctg	ctg	cct	att	cac	act	ctg	agg	ctt	ggt	gtg	gaa	gtg	gat	tcc	ttt	1845
203	Leu	Leu	Pro	Ile	His	Thr	Leu	Arg	Leu	Gly	Val	Glu	Val	Asp	Ser	Phe	
204				565					570					575			
206	gat	ggg	cac	cat	tat	att	tct	tca	att	gtt	tct	ggt	ggt	cct	gtt	gat	1893
207	Asp	Gly	His	His	Tyr	Ile	Ser	Ser	Ile	Val	Ser	Gly	Gly	Pro	Val	Asp	
208			580					585					590				
210	aca	ttg	ggt	ctc	cta	cag	cca	gaa	gat	gag	ctg	ctt	gag	gtc	aat	ggc	1941
211	Thr	Leu	Gly	Leu	Leu	Gln	Pro	Glu	Asp	Glu	Leu	Leu	Glu	Val	Asn	Gly	
212		595					600					605					
214	atg	cag	ctt	tat	gga	aaa	tct	cgc	cga	gaa	gca	gtc	tcc	ttt	ctt	aaa	1989
215	Met	Gln	Leu	Tyr	Gly	Lys	Ser	Arg	Arg	Glu	Ala	Val	Ser	Phe	Leu	Lys	
216	610					615					620					625	
218	gaa	gtg	cca	ccc	cct	ttt	act	ttg	gtt	tgc	tgt	cgg	agg	ttg	ttt	gat	2037
219	Glu	Val	Pro	Pro	Phe	Thr	Leu	Val	Cys	Cys	Arg	Arg	Leu	Phe	Asp		
220				630					635					640			
222	gat	gaa	gct	tct	gta	gat	gaa	cca	agg	cgc	act	gaa	acc	tct	ctt	cct	2085
223	Asp	Glu	Ala	Ser	Val	Asp	Glu	Pro	Arg	Arg	Thr	Glu	Thr	Ser	Leu	Pro	
224				645					650					655			
226	gag	aca	gag	gtt	gac	cac	aat	atg	gat	gtc	aat	act	gaa	gaa	gat	gat	2133
227	Glu	Thr	Glu	Val	Asp	His	Asn	Met	Asp	Val	Asn	Thr	Glu	Glu	Asp	Asp	
228			660						665				670				
230	gat	ggg	gaa	tta	gca	ctg	tgg	tcc	cct	gaa	gtc	aag	att	gtt	gaa	cta	2181
231	Asp	Gly	Glu	Leu	Ala	Leu	Trp	Ser	Pro	Glu	Val	Lys	Ile	Val	Glu	Leu	
232		675				680						685					
234	gta	aaa	gat	tgt	aaa	ggt	ttg	gga	ttc	agc	att	ttg	gat	tac	cag	gac	2229
235	Val	Lys	Asp	Cys	Lys	Gly	Leu	Gly	Phe	Ser	Ile	Leu	Asp	Tyr	Gln	Asp	
236	690					695				700					705		
238	cct	tta	gat	cct	aca	aga	tca	gtg	att	gtg	atc	cgc	tcc	ctg	gta	gca	2277
239	Pro	Leu	Asp	Pro	Thr	Arg	Ser	Val	Ile	Val	Ile	Arg	Ser	Leu	Val	Ala	
240				710						715				720			
242	gat	ggt	gta	gca	gaa	aga	agt	ggg	gga	cta	tta	cct	gga	gac	cgc	ctg	2325
243	Asp	Gly	Val	Ala	Glu	Arg	Ser	Gly	Gly	Leu	Leu	Pro	Gly	Asp	Arg	Leu	
244				725					730					735			
246	gtc	tca	gtc	aat	gaa	tac	tgt	ttg	gac	aac	acc	tca	ctt	gct	gaa	gct	2373
247	Val	Ser	Val	Asn	Glu	Tyr	Cys	Leu	Asp	Asn	Thr	Ser	Leu	Ala	Glu	Ala	
248			740						745					750			
250	gtg	gaa	ata	ttg	aaa	gct	gtg	cca	cca	ggc	cta	gta	cac	ctt	ggc	atc	2421
251	Val	Glu	Ile	Leu	Lys	Ala	Val	Pro	Pro	Gly	Leu	Val	His	Leu	Gly	Ile	
252		755					760						765				
254	tgt	aag	cct	ttg	gtg	gaa	gat	aat	gaa	gaa	gaa	agt	tgt	tat	att	tta	2469
255	Cys	Lys	Pro	Leu	Val	Glu	Asp	Asn	Glu	Glu	Glu	Ser	Cys	Tyr	Ile	Leu	
256	770					775					780					785	
258	cat	tca	agc	agt	aat	gaa	gac	aag	act	gaa	ttt	tca	gga	aca	att	cat	2517
259	His	Ser	Ser	Ser	Asn	Glu	Asp	Lys	Thr	Glu	Phe	Ser	Gly	Thr	Ile	His	

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260		790		795		800	
262	gat ata aat tca tct tta ata ctc gaa gca ccc aag gga ttt aga gat	2565					
263	Asp Ile Asn Ser Ser Leu Ile Leu Glu Ala Pro Lys Gly Phe Arg Asp						
264	805 810 815						
266	gaa cca tat ttt aaa gaa gaa ctt gtg gat gaa cca ttt cta gat ctg	2613					
267	Glu Pro Tyr Phe Lys Glu Glu Leu Val Asp Glu Pro Phe Leu Asp Leu						
268	820 825 830						
270	gga aag tct ttc cat tcc caa caa aaa gag ata gag caa agc aag gag	2661					
271	Gly Lys Ser Phe His Ser Gln Gln Lys Glu Ile Glu Gln Ser Lys Glu						
272	835 840 845						
274	gcc tgg gag atg cat gaa ttt ctg act cct aga ttg cag gaa atg gat	2709					
275	Ala Trp Glu Met His Glu Phe Leu Thr Pro Arg Leu Gln Glu Met Asp						
276	850 855 860 865						
278	gaa gaa aga gaa atg ctt gtt gat gaa gaa tat gag tta tat caa gat	2757					
279	Glu Glu Arg Glu Met Leu Val Asp Glu Glu Tyr Glu Leu Tyr Gln Asp						
280	870 875 880						
282	ccc tca cca tcc atg gag ttg tat ccc ttg tcg cac att caa gag gcc	2805					
283	Pro Ser Pro Ser Met Glu Leu Tyr Pro Leu Ser His Ile Gln Glu Ala						
284	885 890 895						
286	act cct gtg ccc tct gtg aat gaa ctt cac ttt ggt aca cag tgg ttg	2853					
287	Thr Pro Val Pro Ser Val Asn Glu Leu His Phe Gly Thr Gln Trp Leu						
288	900 905 910						
290	cat gat aat gaa cca tcc gag tct caa gag gca aga acc ggg agg act	2901					
291	His Asp Asn Glu Pro Ser Glu Ser Gln Glu Ala Arg Thr Gly Arg Thr						
292	915 920 925						
294	gtc tat tcc cag gag gca cag ccg tat ggc tat tgc cct gaa aat gtg	2949					
295	Val Tyr Ser Gln Glu Ala Gln Pro Tyr Gly Tyr Cys Pro Glu Asn Val						
296	930 935 940 945						
298	atg aaa gaa aat ttt gtc atg gag tcc cta cca tct gta cca tca act	2997					
299	Met Lys Glu Asn Phe Val Met Glu Ser Leu Pro Ser Val Pro Ser Thr						
300	950 955 960						
302	gaa gga aac agt caa caa ggc aga ttt gac gac ctg gaa aat ctt aat	3045					
303	Glu Gly Asn Ser Gln Gln Gly Arg Phe Asp Asp Leu Glu Asn Leu Asn						
304	965 970 975						
306	tca tta gca aaa act agt ctg gat tta ggc atg atc ccg aat gat gtc	3093					
307	Ser Leu Ala Lys Thr Ser Leu Asp Leu Gly Met Ile Pro Asn Asp Val						
308	980 985 990						
310	caa ggt cct agc ttg ctc att gac ctt cct gtt gtg gct caa agg agg	3141					
311	Gln Gly Pro Ser Leu Leu Ile Asp Leu Pro Val Val Ala Gln Arg Arg						
312	995 1000 1005						
314	gag caa gaa gat ttg cct tta tat caa cac caa gcg aca cga gtt att	3189					
315	Glu Gln Glu Asp Leu Pro Leu Tyr Gln His Gln Ala Thr Arg Val Ile						
316	1010 1015 1020 1025						
318	tcc aag gcc tca gca tac aca gga atg ttg tct tct aga tat gcc act	3237					
319	Ser Lys Ala Ser Ala Tyr Thr Gly Met Leu Ser Ser Arg Tyr Ala Thr						
320	1030 1035 1040						
322	gat aca tgt gag tta cct gag aga gaa gaa ggc gaa gga gaa gaa act	3285					
323	Asp Thr Cys Glu Leu Pro Glu Arg Glu Glu Gly Glu Gly Glu Glu Thr						
324	1045 1050 1055						

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; Xaa Pos. 2,3,4

VERIFICATION SUMMARY

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L:42 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0